

## **RAW SEQUENCE LISTING**

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Application Serial Number: 101612, 466B  
Source: TFWU  
Date Processed by STIC: 7-31-05

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IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/612,466B

DATE: 01/31/2005

TIME: 11:50:14

Input Set : A:\1625seq.003

Output Set: N:\CRF4\01312005\J612466B.raw

3 <110> APPLICANT: Madison, Edwin  
4 Ong, Edgar  
5 Yeh, Juinn-Chern  
7 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE 16, THE  
8 ENCODED PROTEINS AND METHODS BASED THEREON  
10 <130> FILE REFERENCE: 24745-1625  
12 <140> CURRENT APPLICATION NUMBER: 10/612,466B  
13 <141> CURRENT FILING DATE: 2003-07-01  
15 <150> PRIOR APPLICATION NUMBER: 60/394,347  
16 <151> PRIOR FILING DATE: 2002-07-02  
18 <160> NUMBER OF SEQ ID NOS: 22  
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 3147  
24 <212> TYPE: DNA  
25 <213> ORGANISM: Homo Sapien  
27 <220> FEATURE:  
28 <221> NAME/KEY: CDS  
29 <222> LOCATION: (23) ... (2589)  
30 <223> OTHER INFORMATION: Nucleotide sequence encoding MTSP1  
32 <300> PUBLICATION INFORMATION:  
33 <308> DATABASE ACCESSION NO: GenBank #AR081724  
34 <309> DATABASE ENTRY DATE: 2000-08-31  
36 <400> SEQUENCE: 1  
37 tcaagagccg cctcgggta cc atg ggg agc gat cg ggc cgc aag ggc gga 52  
38 Met Gly Ser Asp Arg Ala Arg Lys Gly Gly  
39 1 5 10  
41 ggg ggc ccg aag gac ttc ggc gcg gga ctc aag tac aac tcc cg cac 100  
42 Gly Gly Pro Lys Asp Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His  
43 15 20 25  
45 gag aaa gtg aat ggc ttg gag gaa ggc gtg gag ttc ctg cca gtc aac 148  
46 Glu Lys Val Asn Gly Leu Glu Gly Val Glu Phe Leu Pro Val Asn  
47 30 35 40  
49 aac gtc aag aag gtg gaa aag cat ggc ccg ggg cgc tgg gtg gtg ctg 196  
50 Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu  
51 45 50 55  
53 gca gcc gtg ctg atc ggc ctc ctc ttg gtc ttg ctg ggg atc ggc ttc 244  
54 Ala Ala Val Leu Ile Gly Leu Leu Val Leu Leu Gly Ile Gly Phe  
55 60 65 70  
57 ctg gtg tgg cat ttg cag tac cg gac gtg cgt gtc cag aag gtc ttc 292  
58 Leu Val Trp His Leu Gln Tyr Arg Asp Val Arg Val Gln Lys Val Phe  
59 75 80 85 90  
61 aat qgc tac atq aqg atc aca aat qaq aat ttt qtq qat qcc tac qaq 340

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62	Asn	Gly	Tyr	Met	Arg	Ile	Thr	Asn	Glu	Asn	Phe	Val	Asp	Ala	Tyr	Glu	
63				95				100						105			
65	aac	tcc	aac	tcc	act	gag	ttt	gta	agc	ctg	gcc	agc	aag	gtg	aag	gac	388
66	Asn	Ser	Asn	Ser	Thr	Glu	Phe	Val	Ser	Leu	Ala	Ser	Lys	Val	Lys	Asp	
67				110					115				120				
69	gcg	ctg	aag	ctg	ctg	tac	agc	gga	gtc	cca	ttc	ctg	ggc	ccc	tac	cac	436
70	Ala	Leu	Lys	Leu	Leu	Tyr	Ser	Gly	Val	Pro	Phe	Leu	Gly	Pro	Tyr	His	
71				125				130				135					
73	aag	gag	tcg	gct	gtg	acg	gcc	ttc	agc	gag	ggc	agc	gtc	atc	gcc	tac	484
74	Lys	Glu	Ser	Ala	Val	Thr	Ala	Phe	Ser	Glu	Gly	Ser	Val	Ile	Ala	Tyr	
75				140				145				150					
77	tac	tgg	tct	gag	ttc	agc	atc	ccg	cag	cac	ctg	gtg	gag	gag	gcc	gag	532
78	Tyr	Trp	Ser	Glu	Phe	Ser	Ile	Pro	Gln	His	Leu	Val	Glu	Glu	Ala	Glu	
79	155				160				165			170					
81	cgc	gtc	atg	gcc	gag	gag	cgc	gta	gtc	atg	ctg	ccc	ccg	cg	g	cgc	580
82	Arg	Val	Met	Ala	Glu	Glu	Arg	Val	Val	Met	Leu	Pro	Pro	Arg	Ala	Arg	
83				175				180			185						
85	tcc	ctg	aag	tcc	ttt	gtg	gtc	acc	tca	gtg	gtg	gt	tcc	ccc	acg	gac	628
86	Ser	Leu	Lys	Ser	Phe	Val	Val	Thr	Ser	Val	Val	Ala	Phe	Pro	Thr	Asp	
87				190				195			200						
89	tcc	aaa	aca	gta	cag	agg	acc	cag	gac	aac	agc	tgc	agc	ttt	ggc	ctg	676
90	Ser	Lys	Thr	Val	Gln	Arg	Thr	Gln	Asp	Asn	Ser	Cys	Ser	Phe	Gly	Leu	
91				205				210			215						
93	cac	gcc	cgc	ggt	gtg	gag	ctg	atg	cgc	ttc	acc	acg	ccc	ggc	ttc	cct	724
94	His	Ala	Arg	Gly	Val	Glu	Leu	Met	Arg	Phe	Thr	Thr	Pro	Gly	Phe	Pro	
95				220				225			230						
97	gac	agc	ccc	tac	ccc	gct	cat	gcc	cgc	tgc	cag	tgg	gcc	ctg	cg	gg	772
98	Asp	Ser	Pro	Tyr	Pro	Ala	His	Ala	Arg	Cys	Gln	Trp	Ala	Leu	Arg	Gly	
99	235				240				245			250					
101	gac	gcc	gac	tca	gtg	ctg	agc	ctc	acc	ttc	cg	agc	ttt	gac	ctt	g	820
102	Asp	Ala	Asp	Ser	Val	Leu	Ser	Leu	Thr	Phe	Arg	Ser	Phe	Asp	Leu	Ala	
103				255				260			265						
105	tcc	tgc	gac	gag	cgc	ggc	agc	gac	ctg	gtg	acg	gtg	tac	aac	acc	ctg	868
106	Ser	Cys	Asp	Glu	Arg	Gly	Ser	Asp	Leu	Val	Thr	Val	Tyr	Asn	Thr	Leu	
107				270				275			280						
109	agc	ccc	atg	gag	ccc	cac	gcc	ctg	gtg	cag	ttg	tgt	ggc	acc	tac	cct	916
110	Ser	Pro	Met	Glu	Pro	His	Ala	Leu	Val	Gln	Leu	Cys	Gly	Thr	Tyr	Pro	
111				285				290			295						
113	ccc	tcc	tac	aac	ctg	acc	ttc	cac	tcc	tcc	cag	aac	gtc	ctg	ctc	atc	964
114	Pro	Ser	Tyr	Asn	Leu	Thr	Phe	His	Ser	Ser	Gln	Asn	Val	Leu	Leu	Ile	
115				300				305			310						
117	aca	ctg	ata	acc	aac	act	gag	cgg	cg	cat	ccc	ggc	ttt	gag	gcc	acc	1012
118	Thr	Leu	Ile	Thr	Asn	Thr	Glu	Arg	Arg	His	Pro	Gly	Phe	Glu	Ala	Thr	
119	315				320				325			330					
121	tcc	tcc	cag	ctg	c	agg	atg	agc	tg	gt	gga	ggc	cgc	tta	cgt	aaa	1060
122	Phe	Phe	Gln	Leu	Pro	Arg	Met	Ser	Ser	Cys	Gly	Gly	Arg	Leu	Arg	Lys	
123				335				340			345						
125	gcc	cag	ggg	aca	ttc	aac	agc	ccc	tac	tac	cca	ggc	cac	tac	cca	ccc	1108
126	Ala	Gln	Gly	Thr	Phe	Asn	Ser	Pro	Tyr	Tyr	Pro	Gly	His	Tyr	Pro	Pro	

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127	350	355	360	
129	aac att gac tgc aca tgg aac att gag gtg ccc aac aac cag cat gtg			1156
130	Asn Ile Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn Gln His Val			
131	365	370	375	
133	aag gtg agc ttc aaa ttc ttc tac ctg ctg gag ccc ggc gtg cct gcg			1204
134	Lys Val Ser Phe Lys Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala			
135	380	385	390	
137	ggc acc tgc ccc aag gac tac gtg gag atc aat ggg gag aaa tac tgc			1252
138	Gly Thr Cys Pro Lys Asp Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys			
139	395	400	405	410
141	gga gag agg tcc cag ttc gtc gtc acc agc aac aac aag atc aca			1300
142	Gly Glu Arg Ser Gln Phe Val Val Thr Ser Asn Ser Asn Lys Ile Thr			
143	415	420	425	
145	gtt cgc ttc cac tca gat cag tcc tac acc gac acc ggc ttc tta gct			1348
146	Val Arg Phe His Ser Asp Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala			
147	430	435	440	
149	gaa tac ctc tcc tac gac tcc agt gac cca tgc ccg ggg cag ttc acg			1396
150	Glu Tyr Leu Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr			
151	445	450	455	
153	tgc cgc acg ggg cgg tgt atc cgg aag gag ctg cgc tgt gat ggc tgg			1444
154	Cys Arg Thr Gly Arg Cys Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp			
155	460	465	470	
157	gcc gac tgc acc gac cac agc gat gag ctc aac tgc agt tgc gac gcc			1492
158	Ala Asp Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala			
159	475	480	485	490
161	ggc cac cag ttc acg tgc aag aac aag ttc tgc aag ccc ctc ttc tgg			1540
162	Gly His Gln Phe Thr Cys Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp			
163	495	500	505	
165	gtc tgc gac agt gtg aac gac tgc gga gac aac agc gac gag cag ggg			1588
166	Val Cys Asp Ser Val Asn Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly			
167	510	515	520	
169	tgc agt tgt ccg gcc cag acc ttc agg tgt tcc aat ggg aag tgc ctc			1636
170	Cys Ser Cys Pro Ala Gln Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu			
171	525	530	535	
173	tcg aaa agc cag cag tgc aat ggg aag gac gac tgt ggg gac ggg tcc			1684
174	Ser Lys Ser Gln Gln Cys Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser			
175	540	545	550	
177	gac gag gcc tcc tgc ccc aag gtg aac gtc gtc act tgt acc aaa cac			1732
178	Asp Glu Ala Ser Cys Pro Lys Val Asn Val Val Thr Cys Thr Lys His			
179	555	560	565	570
181	acc tac cgc tgc ctc aat ggg ctc tgc ttg agc aag ggc aac cct gag			1780
182	Thr Tyr Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu			
183	575	580	585	
185	tgt gac ggg aag gag gac tgt agc gac ggc tca gat gag aag gac tgc			1828
186	Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys			
187	590	595	600	
189	gac tgt ggg ctg cgg tca ttc acg aga cag gct cgt gtt gtt ggg ggc			1876
190	Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly			
191	605	610	615	

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193 acg gat gcg gat gag ggc gag tgg ccc tgg cag gta agc ctg cat gct	1924
194 Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala	
195 620 625 630	
197 ctg ggc cag ggc cac atc tgc ggt gct tcc ctc atc tct ccc aac tgg	1972
198 Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp	
199 635 640 645 650	
201 ctg gtc tct gcc gca cac tgc tac atc gat gac aga gga ttc agg tac	2020
202 Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr	
203 655 660 665	
205 tca gac ccc acg cag tgg acg gcc ttc ctg ggc ttg cac gac cag agc	2068
206 Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu His Asp Gln Ser	
207 670 675 680	
209 cag cgc agc gcc cct ggg gtg cag gag cgc agg ctc aag cgc atc atc	2116
210 Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu Lys Arg Ile Ile	
211 685 690 695	
213 tcc cac ccc ttc ttc aat gac ttc acc ttc gac tat gac atc gcg ctg	2164
214 Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu	
215 700 705 710	
217 ctg gag ctg gag aaa ccg gca gag tac agc tcc atg gtg cgg ccc atc	2212
218 Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met Val Arg Pro Ile	
219 715 720 725 730	
221 tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc ggc aag gcc atc tgg	2260
222 Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp	
223 735 740 745	
225 gtc acg ggc tgg gga cac acc cag tat gga ggc act ggc gcg ctg atc	2308
226 Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile	
227 750 755 760	
229 ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac	2356
230 Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn	
231 765 770 775	
233 ctc ctg ccg cag cag atc acg ccg cgc atg atg tgc gtg ggc ttc ctc	2404
234 Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu	
235 780 785 790	
237 agc ggc ggc gtg gac tcc tgc cag ggt gat tcc ggg gga ccc ctg tcc	2452
238 Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser	
239 795 800 805 810	
241 agc gtg gag gcg gat ggg cgg atc ttc cag gcc ggt gtg gtg agc tgg	2500
242 Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly Val Val Ser Trp	
243 815 820 825	
245 gga gac ggc tgc gct cag agg aac aag cca ggc gtg tac aca agg ctc	2548
246 Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu	
247 830 835 840	
249 cct ctg ttt cgg gac tgg atc aaa gag aac act ggg gta ta gggggccgggg	2599
250 Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val	
251 845 850 855	
253 ccacccaaat gtgtacaccc tgcggggccac ccacatcgatcca cccccagtgatg caccgcctgca	2659
254 ggctggagac tggaccgctg actgcaccag cggcccccaga acatacactg tgaactcaat	2719
255 ctccagggtct cccaaatctgc ctagaaaaacc tctcgcttcc tcagcctcca aagtggagct	2779
256 gggaggtaga agggaggac actgggtggtt ctactgaccc aactggggc aaaggtttga	2839

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257 agacacagcc tccccggca gccccaaagct gggccgaggc gcgtttgtgt atatctgcct 2899  
 258 cccctgtctg taaggagcag cgggaacgga gcttcggagc ctcctcagtg aagggtgg 2959  
 259 ggctggcggta tctggctgt gggggcccttg ggccacgctc ttgaggaagc ccaggctcg 3019  
 260 aggaccctgg aaaacagacg ggtctgagac tgaattgtt ttaccagtc ccagggtgga 3079  
 261 cttcagtgtg tgtatttggta aaaaatgtt aaacaattta tttctttta aaaaaaaaaa 3139  
 262 aaaaaaaaaa 3147  
 264 <210> SEQ ID NO: 2  
 265 <211> LENGTH: 855  
 266 <212> TYPE: PRT  
 267 <213> ORGANISM: Homo Sapien  
 269 <400> SEQUENCE: 2  
 270 Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Pro Lys Asp Phe  
 271 1 5 10 15  
 272 Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu  
 273 20 25 30  
 274 Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu  
 275 35 40 45  
 276 Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly  
 277 50 55 60  
 278 Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln  
 279 65 70 75 80  
 280 Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile  
 281 85 90 95  
 282 Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu  
 283 100 105 110  
 284 Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr  
 285 115 120 125  
 286 Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr  
 287 130 135 140  
 288 Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser  
 289 145 150 155 160  
 290 Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu  
 291 165 170 175  
 292 Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val  
 293 180 185 190  
 294 Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg  
 295 195 200 205  
 296 Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu  
 297 210 215 220  
 298 Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala  
 299 225 230 235 240  
 300 His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu  
 301 245 250 255  
 302 Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly  
 303 260 265 270  
 304 Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His  
 305 275 280 285  
 306 Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr  
 307 290 295 300

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